
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=12; hr=15; min=15; sec=16; ms=94;]

Validated By CRFValidator v 1.0.3

Application No: 10536802 Version No: 1.0

Input Set:

Output Set:

Started: 2007-12-12 14:53:27.553

Finished: 2007-12-12 14:53:28.026

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 473 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 4

Actual SeqID Count: 4

SEQUENCE LISTING

<110>	Japan Science and Technology Agency Tsukasa SEYA Misako MATSUMOTO Hiroyuki OSHIUMI	
<120>	Novel Adaptor Protein that Binds to Mammalian Toll-Like Receptor and Gene Thereof	3,
<130>	1035-591 / A211-02/PCT	
	10536802 2007-12-12	
<150>	PCT/JP2003/014854	
	2003-11-20	
<150>	JP 2002-349015	
<151>	2002-11-29	
<160>	4	
<170>	MS Word	
<210>	1	
<211>	2460	
<212>	DNA	
<213>	Homo sapiens	
<220>		
<221>	CDS	
<222>	(63)(2198)	
<400>	1	
gtgtg	maaca tgccttcacc acctccagct tctgctgccg gaggctgcac ccacctgtgc 60	
	gcc tgc aca ggc cca tca ctt cct agc gcc ttc gac att cta 107 Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu	
Met		
aat a	a qca qqc caq qac aaq ctc ttq tat ctq aaq cac aaa ctq aaq 155	
,,,,,	a Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys	
01y 111	20 25 30	
acc co	ea ege eca gge tge eag ggg eag gae ete etg eat gee atg gtt 203	
Thr Pi	o Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val	
	35 40 45	
ctc ct	g aag ctg ggc cag gaa act gag gcc agg atc tct cta gag gca 251	
Leu Le	u Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala	
	50 55 60	
ttg aa	ng gec gat geg gtg gec egg etg gtg gee ege eag tgg get gge 299	
Leu Ly	s Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly	

	-	_			_	cca Pro					-				-	347
	-	_	_			ctg Leu	_	-			_	_	_		-	395
						tac Tyr										443
	-	-			_	ggg	-		_	_		-	_			491
_			-		_	ggg Gly 150	-			_			_		_	539
		_		_		cca Pro			_	-	_					587
	_			_		att Ile	-		_	_	-		_			635
_		_	_			ggc	-		-		-	_	_		_	683
_		-				acc Thr	-				_	_		_	_	731
				-	-	ctc Leu 230	-	_	_		_	_	_	_		779
			-			ggc Gly	_	_					_	_		827
_						gcc Ala	_				_		Ē	_		875
					-	gtg Val	-		-	-						923
	_			_	-	cca Pro	_		-							971

_					-			-			ccc Pro 315	_			_	1019
	_	-				-		-		-	cag Gln	_				1067
		-	-	-							aag Lys	_	_			1115
					-						cct Pro					1163
				_		-		_			tcc Ser		_			1211
		_	_			_	_	_			tat Tyr 395					1259
		-		_	_	_			_	_	cgg Arg	_			=	1307
_		-					-		-		ttc Phe	_		-		1355
_		_		_			_	_	_	_	cag Gln	_	_		=	1403
		-									aac Asn		-	_	-	1451
_	-	_		_	, ,			_	_	_	agc Ser 475			_	_	1499
_		_		-	-	-				-	ccc Pro	_		-		1547
-	-	_		-		-	-	-	-	_	ctc Leu			_		1595
	_	_	-			-			-		aag Lys		-			1643
ttc	aag	ccc	cac	agg	ctt	cag	gcc	cga	aag	gcc	atg	tgg	agg	aag	gaa	1691

Phe	Lys	Pro 530	His	Arg	Leu	Gln	Ala 535	Arg	Lys	Ala	Met	Trp 540	Arg	Lys	Glu	
-	-		-	-	ctg Leu		-	_	_			_	-			1739
	_				gca Ala 565	_		T.,	-			-				1787
_		-			cag Gln	_	_	_		_		_		-		1835
	-		-		ttt Phe								-	-	-	1883
				_	gtg Val		-		-	_						1931
	_		-	-	cag Gln	-			_		-		_	-		1979
			-		tcc Ser 645		-		-	-			_		-	2027
		_	_		cca Pro	-			_	-			-			2075
_	_			_	caa Gln							_	_	_	_	2123
_	_		_		aac Asn		_			_	_			_		2171
		_	_	_	cag Gln		_	_	tgad	ccgc	gtg t	cctt	gcct	-g		2218
acca	accto	ggg g	gaaca	accc	ct go	gacco	caggo	c ato	cggcd	cagg	acco	ccata	aga q	gcaco	ccggt	2278
ctgo	cccto	gtg d	ccct	gtgga	ac aç	gtgga	aagat	gaç	ggtca	atct	gcca	acttt	ca ç	ggaca	attgtc	2338
cgg	gagco	cct t	catt	tago	ga ca	aaaa	cgggd	c gcç	gatga	atgc	cctç	ggctt	tc a	agggt	ggtca	2398
gaad	ctgga	ata d	cggt	gttta	ac aa	attco	caato	c tct	ctat	ttc	tggg	gtgaa	agg q	gtctt	ggtgg	2458
+ ~																2460

```
<210> 2
<211> 712
<212> PRT
<213> Homo sapiens
<400> 2
Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly
Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr
                               25
Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
                           40
Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
    50
                      55
Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
                   70
Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
                85
Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
           100
                              105
Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
                          120
Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
   130
             135
Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145
Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
              165
                                 170
Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
           180
                              185
Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
                          200
Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
                      215
                                         220
His Gly Pro Ser Lys Leu Cys Asp Pro Gln Ala Ser Leu Val Pro
225 230 235 240
Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
               245
                                 250
Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
```

265

270

Pro	Gly	Leu 275	Pro	Glu	Val	Ala	Pro 280	Asp	Ala	Thr	Ser	Thr 285	Gly	Leu	Pro
Asp	Thr 290	Pro	Ala	Ala	Pro	Glu 295	Thr	Ser	Thr	Asn	Tyr 300	Pro	Val	Glu	Cys
Thr 305	Glu	Gly	Ser	Ala	Gly 310	Pro	Gln	Ser	Leu	Pro 315	Leu	Pro	Ile	Leu	Glu 320
Pro	Val	Lys	Asn	Pro 325	Суз	Ser	Val	Lys	Asp 330	Gln	Thr	Pro	Leu	Gln 335	Leu
Ser	Val	Glu	Asp 340	Thr	Thr	Ser	Pro	Asn 345	Thr	Lys	Pro	Суз	Pro 350	Pro	Thr
Pro	Thr	Thr 355	Pro	Glu	Thr	Ser	Pro 360	Pro	Pro	Pro	Pro	Pro 365	Pro	Pro	Ser
Ser	Thr 370	Pro	Суз	Ser	Ala	His 375	Leu	Thr	Pro	Ser	Ser 380	Leu	Phe	Pro	Ser
Ser 385	Leu	Glu	Ser	Ser	Ser 390	Glu	Gln	Lys	Phe	Tyr 395	Asn	Phe	Val	Ile	Leu 400
His	Ala	Arg	Ala	Asp 405	Glu	His	Ile	Ala	Leu 410	Arg	Val	Arg	Glu	Lys 415	Leu
Glu	Ala	Leu	Gly 420	Val	Pro	Asp	Gly	Ala 425	Thr	Phe	Суз	Glu	Asp 430	Phe	Gln
Val	Pro	Gly 435	Arg	Gly	Glu	Leu	Ser 440	Cys	Leu	Gln	Asp	Ala 445	Ile	Asp	His
Ser	Ala 450	Phe	Ile	Ile	Leu	Leu 455	Leu	Thr	Ser	Asn	Phe 460	Asp	Суз	Arg	Leu
Ser 465	Leu	His	Gln	Val	Asn 470	Gln	Ala	Met	Met	Ser 475	Asn	Leu	Thr	Arg	Gln 480
Gly	Ser	Pro	Asp	Cys 485	Val	Ile	Pro	Phe	Leu 490	Pro	Leu	Glu	Ser	Ser 495	Pro
Ala	Gln	Leu	Ser 500	Ser	Asp	Thr	Ala	Ser 505	Leu	Leu	Ser	Gly	Leu 510	Val	Arg
Leu	Asp	Glu 515	His	Ser	Gln	Ile	Phe 520	Ala	Arg	Lys	Val	Ala 525	Asn	Thr	Phe
Lys	Pro 530	His	Arg	Leu	Gln	Ala 535	Arg	Lys	Ala	Met	Trp 540	Arg	Lys	Glu	Gln
Asp 545	Thr	Arg	Ala	Leu	Arg 550	Glu	Gln	Ser	Gln	His 555	Leu	Asp	Gly	Glu	Arg 560
Met	Gln	Ala	Ala	Ala	Leu	Asn	Ala	Ala	Tyr	Ser	Ala	Tyr	Leu	Gln	Ser

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly 580 585 590
Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro 595 600 605
Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp 610 625
Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr 625 630 635 640
Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro 645 650 655
Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln 660 665 670
Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln 675 680 685
Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro 690 695 700
Glu Asp Lys Thr Gln Glu Ala Glu 705 710
<210> 3 <211> 2299 <212> DNA <213> Mus musculus
<220> <221> CDS <222> (66)(2261)
<400> 3 tcggttcgga acatgtctcc acccacccca ccctctgtgg ctccaggctt cattctccc 60
catec atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc att cta 110 Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu 1 5 10 15
ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag ctg ggg 158 Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly 20 25 30
agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc atg gta 206 Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val 35 40 45
ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg gag tcc 254 Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser 50 55 60

ttg	aag	atg	aac	aca	gta	gcc	cag	ctg	gta	gcc	cac	cag	tgg	gca	gac	302
Leu	Lys	Met	Asn	Thr	Val	Ala	Gln	Leu	Val	Ala	His	Gln	Trp	Ala	Asp	
	65					70					75					
atg	gag	acc	aca	gag	ggc	cct	gag	gag	cct	cca	gac	ttg	tcc	tgg	acg	350
Met	Glu	Thr	Thr	Glu	Gly	Pro	Glu	Glu	Pro	Pro	Asp	Leu	Ser	Trp	Thr	
80					85					90						